

SEQUENCE LISTING

<110> Kobilka, Brian K.
Ghanouni, Pejman
Lee, Tae Weon

<120> Conformational assays to detect binding
to membrane spanning, signal-transducing proteins

<130> STAN-213CIP

<140> Unassigned

<141> 2003-10-22

<150> PCT/US02/13250

<151> 2002-04-24

<150> 09/935,061

<151> 2001-08-21

<150> 60/286,250

<151> 2001-04-24

<160> 22

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> epitope tag peptide

<400> 1

Asp Tyr Lys Asp Asp Asp Asp Lys

1

5

<210> 2

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> epitope tag peptide

<400> 2

Asp Tyr Lys Asp Glu Asp Asp Lys

1

5

<210> 3

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> epitope tag peptide

<400> 3

Ala Trp Arg His Pro Gln Phe Gly Gly

1

5

<210> 4

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> epitope tag peptide

<400> 4

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ile Glu Gly Arg

1

5

10

<210> 5

<211> 1239

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1239)

<400> 5

atg ggg caa ccc ggg aac ggc agc gcc ttc ttg ctg gca ccc aat aga

48

Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg

1

5

10

15

agc cat gcg ccg gac cac gac gtc acg cag caa agg gac gag gtg tgg

96

Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp

20

25

30

gtg gtg ggc atg ggc atc gtc atg tct ctc atc gtc ctg gcc atc gtg

144

Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val

35

40

45

ttt ggc aat gtg ctg gtc atc aca gcc att gcc aag ttc gag cgt ctg

192

Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu

50

55

60

cag acg gtc acc aac tac ttc atc act tca ctg gcc tgt gct gat ctg

240

Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu

65

70

75

80

gtc atg ggc ctg gca gtg gtg ccc ttt ggg gcc gcc cat att ctt atg

288

Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met

85

90

95

aaa atg tgg act ttt ggc aac ttc tgg tgc gag ttt tgg act tcc att

336

Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile

100

105

110

gat gtg ctg tgc gtc acg gct agc att gag acc ctg tgc gtg atc gca

384

Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala

115

120

125

gtg gat cgc tac ttt gcc att act tca cct ttc aag tac cag agc ctg	432
Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu	
130 135 140	
ctg acc aag aat aag gcc cgg gtg atc att ctg atg gtg tgg att gtg	480
Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val	
145 150 155 160	
tca ggc ctt acc tcc ttc ttg ccc att cag atg cac tgg tac cgg gcc	528
Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala	
165 170 175	
acc cac cag gaa gcc atc aac tgc tat gcc aat gag acc tgc tgt gac	576
Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp	
180 185 190	
ttc ttc acg aac caa gcc tat gcc att gcc tct tcc atc gtg tcc ttc	624
Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe	
195 200 205	
tac gtt ccc ctg gtg atc atg gtc ttc gtc tac tcc agg gtc ttt cag	672
Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln	
210 215 220	
gag gcc aaa agg cag ctc cag aag att gac aaa tct gag ggc cgc ttc	720
Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe	
225 230 235 240	
cat gtc cag aac ctt agc cag gtg gag cag gat ggg cgg acg ggg cat	768
His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His	
245 250 255	
gga ctc cgc aga tct tcc aag ttc tgc ttg aag gag cac aaa gcc ctc	816
Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu	
260 265 270	
aag acg tta ggc atc atc atg ggc act ttc acc ctc tgc tgg ctg ccc	864
Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro	
275 280 285	
ttc ttc atc gtt aac att gtg cat gtg atc cag gat aac ctc atc cgt	912
Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg	
290 295 300	
aag gaa gtt tac atc ctc cta aat tgg ata ggc tat gtc aat tct ggt	960
Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly	
305 310 315 320	
ttc aat ccc ctt atc tac tgc cgg agc cca gat ttc agg att gcc ttc	1008
Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe	
325 330 335	
cag gag ctc ctg tgc ctg cgc agg tct tct ttg aag gcc tat ggg aat	1056
Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn	
340 345 350	
ggc tac tcc agc aac ggc aac aca ggg gag cag agt gga tat cac gtg	1104
Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val	
355 360 365	

gaa cag gag aaa gaa aat aaa ctg ctg tgt gaa gac ctc cca ggc acg	1152
Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr	
370 375 380	

gaa gac ttt gtg ggc cat caa ggt act gtg cct agc gat aac att gat	1200
Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp	
385 390 395 400	

tca caa ggg agg aat tgt agt aca aat gac tca ctg ctg	1239
Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu	
405 410	

<210> 6
 <211> 413
 <212> PRT
 <213> Homo sapiens

<400> 6	
Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg	
1 5 10 15	
Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp	
20 25 30	
Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val	
35 40 45	
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu	
50 55 60	
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu	
65 70 75 80	
Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met	
85 90 95	
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile	
100 105 110	
Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala	
115 120 125	
Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu	
130 135 140	
Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val	
145 150 155 160	
Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala	
165 170 175	
Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp	
180 185 190	
Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe	
195 200 205	
Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln	
210 215 220	
Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe	
225 230 235 240	
His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His	
245 250 255	
Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu	
260 265 270	
Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro	
275 280 285	
Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg	
290 295 300	
Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly	

305		310		315		320
Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe						
	325			330		335
Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn						
	340		345			350
Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val						
	355		360			365
Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr						
	370		375			380
Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp						
385		390		395		400
Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu						
	405		410			

<210> 7

<211> 1239

<212> DNA

<213> Artificial Sequence

<220>

<223> Beta-2 Adrenergic Receptor with TEV site in 2nd intracellular loop

<221> CDS

<222> (1)...(1239)

<400> 7

atg ggg caa ccc ggg aac ggc agc gcc ttc ttg ctg gca ccc aat aga	48
Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg	
1 5 10 15	

agc cat gcg ccg gac cac gac gtc acg cag caa agg gac gag gtg tgg	96
Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp	
20 25 30	

gtg gtg ggc atg ggc atc gtc atg tct ctc atc gtc ctg gcc atc gtg	144
Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val	
35 40 45	

ttt ggc aat gtg ctg gtc atc aca gcc att gcc aag ttc gag cgt ctg	192
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu	
50 55 60	

cag acg gtc acc aac tac ttc atc act tca ctg gcc tgt gct gat ctg	240
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu	
65 70 75 80	

gtc atg ggc ctg gca gtg gtg ccc ttt ggg gcc gcc cat att ctt atg	288
Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met	
85 90 95	

aaa atg tgg act ttt ggc aac ttc tgg tgc gag ttt tgg act tcc att	336
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile	
100 105 110	

gat gtg ctg tgc gtc acg gct agc att gag acc ctg tgc gtg atc gca	384
Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala	
115 120 125	

gtg gat cgc tac ttt gcc att act tca cct ttc aag tac cag agc ctg	432
Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu	
130 135 140	
ctg acc aag aat aag gcc cgg gtg atc att ctg atg gtg tgg att gtg	480
Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val	
145 150 155 160	
tca ggc ctt acc tcc ttc ttg ccc att cag atg cac tgg tac cgg gcc	528
Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala	
165 170 175	
acc cac cag gaa gcc atc aac tgc tat gcc aat gag acc tgc tgt gac	576
Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp	
180 185 190	
ttc ttc acg aac caa gcc tat gcc att gcc tct tcc atc gtg tcc ttc	624
Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe	
195 200 205	
tac gtt ccc ctg gtg atc atg gtc ttc gtc tac tcc agg gtc ttt cag	672
Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln	
210 215 220	
gag gcc aaa agg cag ctc cag aag att gac aaa tct gag ggc cgc ttc	720
Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe	
225 230 235 240	
cat gtc cag aac ctt agc cag gtg gag cag gat ggg cgg acg ggg cat	768
His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His	
245 250 255	
gga ctc gaa aac ctc tac ttc cag ggg ttg aag gag cac aaa gcc ctc	816
Gly Leu Glu Asn Leu Tyr Phe Gln Gly Leu Lys Glu His Lys Ala Leu	
260 265 270	
aag acg tta ggc atc atc atg ggc act ttc acc ctc tgc tgg ctg ccc	864
Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro	
275 280 285	
ttc ttc atc gtt aac att gtg cat gtg atc cag gat aac ctc atc cgt	912
Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg	
290 295 300	
aag gaa gtt tac atc ctc cta aat tgg ata ggc tat gtc aat tct ggt	960
Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly	
305 310 315 320	
ttc aat ccc ctt atc tac tgc cgg agc cca gat ttc agg att gcc ttc	1008
Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe	
325 330 335	
cag gag ctc ctg tgc ctg cgc agg tct tct ttg aag gcc tat ggg aat	1056
Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn	
340 345 350	
ggc tac tcc agc aac ggc aac aca ggg gag cag agt gga tat cac gtg	1104
Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val	
355 360 365	

gaa cag gag aaa gaa aat aaa ctg ctg tgt gaa gac ctc cca ggc acg 1152
 Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr
 370 375 380

gaa gac ttt gtg ggc cat caa ggt act gtg cct agc gat aac att gat 1200
 Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp
 385 390 395 400

tca caa ggg agg aat tgt agt aca aat gac tca ctg ctg 1239
 Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu
 405 410

<210> 8

<211> 413

<212> PRT

<213> Artificial Sequence

<220>

<223> Beta-2 Adrenèrgic Receptor with TEV site in 2nd
 intracellular loop

<400> 8

Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg
 1 5 10 15
 Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp
 20 25 30
 Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val
 35 40 45
 Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu
 50 55 60
 Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu
 65 70 75 80
 Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met
 85 90 95
 Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile
 100 105 110
 Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala
 115 120 125
 Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu
 130 135 140
 Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val
 145 150 155 160
 Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala
 165 170 175
 Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp
 180 185 190
 Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe
 195 200 205
 Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln
 210 215 220
 Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe
 225 230 235 240
 His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly Arg Thr Gly His
 245 250 255
 Gly Leu Glu Asn Leu Tyr Phe Gln Gly Leu Lys Glu His Lys Ala Leu
 260 265 270
 Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro

	275		280		285
Phe	Phe Ile Val Asn Ile Val His Val Ile Gln Asp Asn Leu Ile Arg				
	290		295		300
Lys	Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr Val Asn Ser Gly				
305		310		315	320
Phe	Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe				
	325		330		335
Gln	Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn				
	340		345		350
Gly	Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val				
	355		360		365
Glu	Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr				
	370		375		380
Glu	Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp				
385		390		395	400
Ser	Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu				
	405		410		

<210> 9

<211> 1251

<212> DNA

<213> Artificial Sequence

<220>

<223> Beta-2 Adrenergic Receptor with TEV site in 3rd intracellular loop

<221> CDS

<222> (1)...(1251)

<400> 9

atg ggg caa ccc ggg aac ggc agc gcc ttc ttg ctg gca ccc aat aga	48
Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg	
1 5 10 15	

agc cat gcg ccg gac cac gac gtc acg cag caa agg gac gag gtg tgg	96
Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp	
20 25 30	

gtg gtg ggc atg ggc atc gtc atg tct ctc atc gtc ctg gcc atc gtg	144
Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val	
35 40 45	

ttt ggc aat gtg ctg gtc atc aca gcc att gcc aag ttc gag cgt ctg	192
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu	
50 55 60	

cag acg gtc acc aac tac ttc atc act tca ctg gcc tgt gct gat ctg	240
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu	
65 70 75 80	

gtc atg ggc ctg gca gtg gtg ccc ttt ggg gcc gcc cat att ctt atg	288
Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met	
85 90 95	

aaa atg tgg act ttt ggc aac ttc tgg tgc gag ttt tgg act tcc att	336
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile	
100 105 110	

gat gtg ctg tgc gtc acg gct agc att gag acc ctg tgc gtg atc gca Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala 115 120 125	384
gtg gat cgc tac ttt gcc att act tca cct ttc aag gag aat ctc tac Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Glu Asn Leu-Tyr 130 135 140	432
ttc cag ggc ctg ctg acc aag aat aag gcc cgg gtg atc att ctg atg Phe Gln Gly Leu Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met 145 150 155 160	480
gtg tgg att gtg tca ggc ctt acc tcc ttc ttg ccc att cag atg cac Val Trp Ile Val Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His 165 170 175	528
tgg tac cgg gcc acc cac cag gaa gcc atc aac tgc tat gcc aat gag Trp Tyr Arg Ala Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu 180 185 190	576
acc tgc tgt gac ttc ttc acg aac caa gcc tat gcc att gcc tct tcc Thr Cys Cys Asp Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser 195 200 205	624
atc gtg tcc ttc tac gtt ccc ctg gtg atc atg gtc ttc gtc tac tcc Ile Val Ser Phe Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser 210 215 220	672
agg gtc ttt cag gag gcc aaa agg cag ctc cag aag att gac aaa tct Arg Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser 225 230 235 240	720
gag ggc cgc ttc cat gtc cag aac ctt agc cag gtg gag cag gat ggg Glu Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly 245 250 255	768
cgg acg ggg cat gga ctc cgc aga tct tcc aag ttc tgc ttg aag gag Arg Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu 260 265 270	816
cac aaa gcc ctc aag acg tta ggc atc atc atg ggc act ttc acc ctc His Lys Ala Leu Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu 275 280 285	864
tgc tgg ctg ccc ttc ttc atc gtt aac att gtg cat gtg atc cag gat Cys Trp Leu Pro Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp 290 295 300	912
aac ctc atc cgt aag gaa gtt tac atc ctc cta aat tgg ata ggc tat Asn Leu Ile Arg Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr 305 310 315 320	960
gtc aat tct ggt ttc aat ccc ctt atc tac tgc cgg agc cca gat ttc Val Asn Ser Gly Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe 325 330 335	1008
agg att gcc ttc cag gag ctc ctg tgc ctg cgc agg tct tct ttg aag Arg Ile Ala Phe Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys 340 345 350	1056

gcc tat ggg aat ggc tac tcc agc aac ggc aac aca ggg gag cag agt	1104
Ala Tyr Gly Asn Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser	
355 360 365	
gga tat cac gtg gaa cag gag aaa gaa aat aaa ctg ctg tgt gaa gac	1152
Gly Tyr His Val Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp	
370 375 380	
ctc cca ggc acg gaa gac ttt gtg ggc cat caa ggt act gtg cct agc	1200
Leu Pro Gly Thr Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser	
385 390 395 400	
gat aac att gat tca caa ggg agg aat tgt agt aca aat gac tca ctg	1248
Asp Asn Ile Asp Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu	
405 410 415	
ctg	1251
Leu	

<210> 10
 <211> 417
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Beta-2 Adrenergic Receptor with TEV site in 3rd
 intracellular loop

<400> 10

Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Pro Asn Arg	
1 5 10 15	
Ser His Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp	
20 25 30	
Val Val Gly Met Gly Ile Val Met Ser Leu Ile Val Leu Ala Ile Val	
35 40 45	
Phe Gly Asn Val Leu Val Ile Thr Ala Ile Ala Lys Phe Glu Arg Leu	
50 55 60	
Gln Thr Val Thr Asn Tyr Phe Ile Thr Ser Leu Ala Cys Ala Asp Leu	
65 70 75 80	
Val Met Gly Leu Ala Val Val Pro Phe Gly Ala Ala His Ile Leu Met	
85 90 95	
Lys Met Trp Thr Phe Gly Asn Phe Trp Cys Glu Phe Trp Thr Ser Ile	
100 105 110	
Asp Val Leu Cys Val Thr Ala Ser Ile Glu Thr Leu Cys Val Ile Ala	
115 120 125	
Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Glu Asn Leu Tyr	
130 135 140	
Phe Gln Gly Leu Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met	
145 150 155 160	
Val Trp Ile Val Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His	
165 170 175	
Trp Tyr Arg Ala Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu	
180 185 190	
Thr Cys Cys Asp Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser	
195 200 205	
Ile Val Ser Phe Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser	

210	215	220
Arg Val Phe Gln Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser		
225	230	235
Glu Gly Arg Phe His Val Gln Asn Leu Ser Gln Val Glu Gln Asp Gly		240
	245	250
Arg Thr Gly His Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu		255
	260	265
His Lys Ala Leu Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu		270
	275	280
Cys Trp Leu Pro Phe Phe Ile Val Asn Ile Val His Val Ile Gln Asp		285
290	295	300
Asn Leu Ile Arg Lys Glu Val Tyr Ile Leu Leu Asn Trp Ile Gly Tyr		305
	310	315
Val Asn Ser Gly Phe Asn Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe		320
	325	330
Arg Ile Ala Phe Gln Glu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys		335
	340	345
Ala Tyr Gly Asn Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser		350
	355	360
Gly Tyr His Val Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp		365
	370	375
Leu Pro Gly Thr Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser		380
385	390	395
Asp Asn Ile Asp Ser Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu		400
	405	410
		415
Leu		

<210> 11
 <211> 1176
 <212> DNA
 <213> homo sapiens

<220>
 <221> CDS
 <222> (1)...(1176)

<400> 11	
atg gac agc agc gct gcc ccc acg aac gcc agc aat tgc act gat gcc	48
Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala	
1 5 10 15	
ttg gcg tac tca agt tgc tcc cca gca ccc agc ccc ggt tcc tgg gtc	96
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val	
20 25 30	
aac ttg tcc cac tta gat ggc gac ctg tcc gac cca tgc ggt ccg aac	144
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn	
35 40 45	
cgc acc gac ctg ggc ggg aga gac agc ctg tgc cct cca acc ggc agt	192
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser	
50 55 60	
ccc tcc atg atc acg gcc atc acg atc atg gcc ctc tac tcc atc gtg	240
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val	
65 70 75 80	
tgc gtg gtg ggg ctc ttc gga aac ttc ctg gtc atg tat gtg att gtc	288

Cys	Val	Val	Gly	Leu	Phe	Gly	Asn	Phe	Leu	Val	Met	Tyr	Val	Ile	Val		
				85					90					95			
aga	tac	acc	aag	atg	aag	act	gcc	acc	aac	atc	tac	att	ttc	aac	ctt	336	
Arg	Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu		
			100					105					110				
gct	ctg	gca	gat	gcc	tta	gcc	acc	agt	acc	ctg	ccc	ttc	cag	agt	gtg	384	
Ala	Leu	Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Val		
		115					120					125					
aat	tac	cta	atg	gga	aca	tgg	cca	ttt	gga	acc	atc	ctt	tgc	aag	ata	432	
Asn	Tyr	Leu	Met	Gly	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile		
	130					135					140						
gtg	atc	tcc	ata	gat	tac	tat	aac	atg	ttc	acc	agc	ata	ttc	acc	ctc	480	
Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu		
145					150					155					160		
tgc	acc	atg	agt	gtt	gat	cga	tac	att	gca	gtc	tgc	cac	cct	gtc	aag	528	
Cys	Thr	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys		
				165					170					175			
gcc	tta	gat	ttc	cgt	act	ccc	cga	aat	gcc	aaa	att	atc	aat	gtc	tgc	576	
Ala	Leu	Asp	Phe	Arg	Thr	Pro	Arg	Asn	Ala	Lys	Ile	Ile	Asn	Val	Cys		
			180					185					190				
aac	tgg	atc	ctc	tct	tca	gcc	att	ggg	ctt	cct	gta	atg	ttc	ata	gct	624	
Asn	Trp	Ile	Leu	Ser	Ser	Ala	Ile	Gly	Leu	Pro	Val	Met	Phe	Ile	Ala		
		195					200					205					
aca	aca	aaa	tac	agg	caa	ggg	tcc	ata	gat	tgt	aca	cta	aca	ttc	tct	672	
Thr	Thr	Lys	Tyr	Arg	Gln	Gly	Ser	Ile	Asp	Cys	Thr	Leu	Thr	Phe	Ser		
		210				215					220						
cat	cca	acc	tgg	tac	tgg	gaa	aac	ctg	ctg	aag	atc	tgt	gtt	ttc	atc	720	
His	Pro	Thr	Trp	Tyr	Trp	Glu	Asn	Leu	Leu	Lys	Ile	Cys	Val	Phe	Ile		
225					230					235					240		
ttc	gcc	ttc	att	atg	cca	gtg	ctc	atc	att	acc	gtg	tgc	tat	gga	ctg	768	
Phe	Ala	Phe	Ile	Met	Pro	Val	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu		
				245				250						255			
atg	atc	ttg	cgc	ctc	aag	agt	gtc	cgc	atg	ctc	tct	ggc	tcc	aaa	gaa	816	
Met	Ile	Leu	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu		
			260					265					270				
aag	gac	agg	aat	ctt	cga	agg	atc	acc	agg	atg	gtg	ctg	gtg	gtg	gtg	864	
Lys	Asp	Arg	Asn	Leu	Arg	Arg	Ile	Thr	Arg	Met	Val	Leu	Val	Val	Val		
		275					280					285					
gct	gtg	ttc	atc	gtc	tgc	tgg	act	ccc	att	cac	att	tac	gtc	atc	att	912	
Ala	Val	Phe	Ile	Val	Cys	Trp	Thr	Pro	Ile	His	Ile	Tyr	Val	Ile	Ile		
		290				295					300						
aaa	gcc	ttg	gtt	aca	atc	cca	gaa	act	acg	ttc	cag	act	gtt	tct	tgg	960	
Lys	Ala	Leu	Val	Thr	Ile	Pro	Glu	Thr	Thr	Phe	Gln	Thr	Val	Ser	Trp		
305					310					315					320		

cac ttc tgc att gct cta ggt tac aca aac agc tgc ctc aac cca gtc	1008
His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val	
325 330 335	
ctt tat gca ttt ctg gat gaa aac ttc aaa cga tgc ttc aga gag ttc	1056
Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe	
340 345 350	
tgt atc cca acc tct tcc aac att gag caa caa aac tcc act cga att	1104
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile	
355 360 365	
cgt cag aac act aga gac cac ccc tcc acg gcc aat aca gtg gat aga	1152
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg	
370 375 380	
act aat cat cag gta cgc agt ctc	1176
Thr Asn His Gln Val Arg Ser Leu	
385 390	

<210> 12
 <211> 392
 <212> PRT
 <213> homo sapiens

<400> 12

Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala	
1 5 10 15	
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val	
20 25 30	
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn	
35 40 45	
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser	
50 55 60	
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val	
65 70 75 80	
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val	
85 90 95	
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu	
100 105 110	
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val	
115 120 125	
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile	
130 135 140	
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu	
145 150 155 160	
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys	
165 170 175	
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys	
180 185 190	
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala	
195 200 205	
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser	
210 215 220	
His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile	
225 230 235 240	
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu	
245 250 255	

Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
 260 265 270
 Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
 275 280 285
 Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
 290 295 300
 Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
 305 310 315 320
 His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
 325 330 335
 Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
 340 345 350
 Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
 355 360 365
 Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
 370 375 380
 Thr Asn His Gln Val Arg Ser Leu
 385 390

<210> 13

<211> 1176

<212> DNA

<213> Artificial Sequence

<220>

<223> ' Opioid receptor with TEV site in 2nd
intracellular loop

<221> CDS

<222> (1)...(1176)

<400> 13

atg gac agc agc gct gcc ccc acg aac gcc agc aat tgc act gat gcc 48
 Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
 1 5 10 15

ttg gcg tac tca agt tgc tcc cca gca ccc agc ccc ggt tcc tgg gtc 96
 Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
 20 25 30

aac ttg tcc cac tta gat ggc gac ctg tcc gac cca tgc ggt ccg aac 144
 Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn
 35 40 45

cgc acc gac ctg ggc ggg aga gac agc ctg tgc cct cca acc ggc agt 192
 Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
 50 55 60

ccc tcc atg atc acg gcc atc acg atc atg gcc ctc tac tcc atc gtg 240
 Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
 65 70 75 80

tgc gtg gtg ggg ctc ttc gga aac ttc ctg gtc atg tat gtg att gtc 288
 Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
 85 90 95

aga tac acc aag atg aag act gcc acc aac atc tac att ttc aac ctt 336
 Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
 100 105 110

gct ctg gca gat gcc tta gcc acc agt acc ctg ccc ttc cag agt gtg Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val 115 120 125	384
aat tac cta atg gga aca tgg cca ttt gga acc atc ctt tgc aag ata Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile 130 135 140	432
gtg atc tcc ata gat tac tat aac atg ttc acc agc ata ttc acc ctc Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu 145 150 155 160	480
tgc acc atg agt gtt gat cga tac att gca gtc tgc cac cct gtc aag Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys 165 170 175	528
gaa aac ctc tac ttc cag ggg cga aat gcc aaa att atc aat gtc tgc Glu Asn Leu Tyr Phe Gln Gly Arg Asn Ala Lys Ile Ile Asn Val Cys 180 185 190	576
aac tgg atc ctc tct tca gcc att ggt ctt cct gta atg ttc ata gct Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala 195 200 205	624
aca aca aaa tac agg caa ggt tcc ata gat tgt aca cta aca ttc tct Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser 210 215 220	672
cat cca acc tgg tac tgg gaa aac ctg ctg aag atc tgt gtt ttc atc His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile 225 230 235 240	720
ttc gcc ttc att atg cca gtg ctc atc att acc gtg tgc tat gga ctg Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu 245 250 255	768
atg atc ttg cgc ctc aag agt gtc cgc atg ctc tct ggc tcc aaa gaa Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu 260 265 270	816
aag gac agg aat ctt cga agg atc acc agg atg gtg ctg gtg gtg gtg Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val 275 280 285	864
gct gtg ttc atc gtc tgc tgg act ccc att cac att tac gtc atc att Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile 290 295 300	912
aaa gcc ttg gtt aca atc cca gaa act acg ttc cag act gtt tct tgg Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp 305 310 315 320	960
cac ttc tgc att gct cta ggt tac aca aac agc tgc ctc aac cca gtc His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val 325 330 335	1008
ctt tat gca ttt ctg gat gaa aac ttc aaa cga tgc ttc aga gag ttc Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe 1056	

340	345	350	
tgt atc cca acc tct tcc aac att gag caa caa aac tcc act cga att			1104
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile			
355	360	365	
cg t cag aac act aga gac cac ccc tcc acg gcc aat aca gtg gat aga			1152
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg			
370	375	380	
act aat cat cag gta cgc agt ctc			1176
Thr Asn His Gln Val Arg Ser Leu			
385	390		

<210> 14
 <211> 392
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ' Opioid receptor with TEV site in 2nd
 intracellular loop

<400> 14

Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala			
1	5	10	15
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val			
20	25	30	
Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn			
35	40	45	
Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser			
50	55	60	
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val			
65	70	75	80
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val			
85	90	95	
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu			
100	105	110	
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val			
115	120	125	
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile			
130	135	140	
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu			
145	150	155	160
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys			
165	170	175	
Glu Asn Leu Tyr Phe Gln Gly Arg Asn Ala Lys Ile Ile Asn Val Cys			
180	185	190	
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Ile Ala			
195	200	205	
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser			
210	215	220	
His Pro Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile			
225	230	235	240
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu			
245	250	255	
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu			
260	265	270	

Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
 275 280 285
 Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
 290 295 300
 Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
 305 310 315 320
 His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
 325 330 335
 Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
 340 345 350
 Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
 355 360 365
 Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
 370 375 380
 Thr Asn His Gln Val Arg Ser Leu
 385 390

<210> 15

<211> 1197

<212> DNA

<213> Artificial Sequence

<220>

<223> ' Opioid receptor with TEV site in 3rd
intracellular loop

<221> CDS

<222> (1)...(1197)

<400> 15

atg gac agc agc gct gcc ccc acg aac gcc agc aat tgc act gat gcc 48
 Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
 1 5 10 15

ttg gcg tac tca agt tgc tcc cca gca ccc agc ccc ggt tcc tgg gtc 96
 Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
 20 25 30

aac ttg tcc cac tta gat ggc gac ctg tcc gac cca tgc ggt ccg aac 144
 Asn Leu Ser His Leu Asp Gly Asp Leu Ser Asp Pro Cys Gly Pro Asn
 35 40 45

cgc acc gac ctg ggc ggg aga gac agc ctg tgc cct cca acc ggc agt 192
 Arg Thr Asp Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
 50 55 60

ccc tcc atg atc acg gcc atc acg atc atg gcc ctc tac tcc atc gtg 240
 Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
 65 70 75 80

tgc gtg gtg ggg ctc ttc gga aac ttc ctg gtc atg tat gtg att gtc 288
 Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
 85 90 95

aga tac acc aag atg aag act gcc acc aac atc tac att ttc aac ctt 336
 Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
 100 105 110

gct ctg gca gat gcc tta gcc acc agt acc ctg ccc ttc cag agt gtg 384

Ala	Leu	Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Val		
	115						120					125					
aat	tac	cta	atg	gga	aca	tgg	cca	ttt	gga	acc	atc	ctt	tgc	aag	ata	432	
Asn	Tyr	Leu	Met	Gly	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile		
	130					135					140						
gtg	atc	tcc	ata	gat	tac	tat	aac	atg	ttc	acc	agc	ata	ttc	acc	ctc	480	
Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu		
	145				150					155					160		
tgc	acc	atg	agt	gtt	gat	cga	tac	att	gca	gtc	tgc	cac	cct	gtc	aag	528	
Cys	Thr	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys		
				165					170					175			
gcc	tta	gat	ttc	cgt	act	ccc	cga	aat	gcc	aaa	att	atc	aat	gtc	tgc	576	
Ala	Leu	Asp	Phe	Arg	Thr	Pro	Arg	Asn	Ala	Lys	Ile	Ile	Asn	Val	Cys		
			180					185					190				
aac	tgg	atc	ctc	tct	tca	gcc	att	ggg	ctt	cct	gta	atg	ttc	ata	gct	624	
Asn	Trp	Ile	Leu	Ser	Ser	Ala	Ile	Gly	Leu	Pro	Val	Met	Phe	Ile	Ala		
	195						200					205					
aca	aca	aaa	tac	agg	caa	ggg	tcc	ata	gat	tgt	aca	cta	aca	ttc	tct	672	
Thr	Thr	Lys	Tyr	Arg	Gln	Gly	Ser	Ile	Asp	Cys	Thr	Leu	Thr	Phe	Ser		
	210					215					220						
cat	cca	acc	tgg	tac	tgg	gaa	aac	ctg	ctg	aag	atc	tgt	gtt	ttc	atc	720	
His	Pro	Thr	Trp	Tyr	Trp	Glu	Asn	Leu	Leu	Lys	Ile	Cys	Val	Phe	Ile		
	225				230					235					240		
ttc	gcc	ttc	att	atg	cca	gtg	ctc	atc	att	acc	gtg	tgc	tat	gga	ctg	768	
Phe	Ala	Phe	Ile	Met	Pro	Val	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu		
				245					250					255			
atg	atc	ttg	cgc	ctc	aag	agt	gtc	cgc	atg	ctc	tct	ggc	tcc	aaa	gaa	816	
Met	Ile	Leu	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu		
			260					265					270				
aag	gac	gaa	aac	ctc	tac	ttc	cag	ggg	agg	aat	ctt	cga	agg	atc	acc	864	
Lys	Asp	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Arg	Asn	Leu	Arg	Arg	Ile	Thr		
	275						280					285					
agg	atg	gtg	ctg	gtg	gtg	gtg	gct	gtg	ttc	atc	gtc	tgc	tgg	act	ccc	912	
Arg	Met	Val	Leu	Val	Val	Val	Ala	Val	Phe	Ile	Val	Cys	Trp	Thr	Pro		
	290					295					300						
att	cac	att	tac	gtc	atc	att	aaa	gcc	ttg	gtt	aca	atc	cca	gaa	act	960	
Ile	His	Ile	Tyr	Val	Ile	Ile	Lys	Ala	Leu	Val	Thr	Ile	Pro	Glu	Thr		
	305				310					315					320		
acg	ttc	cag	act	gtt	tct	tgg	cac	ttc	tgc	att	gct	cta	ggg	tac	aca	1008	
Thr	Phe	Gln	Thr	Val	Ser	Trp	His	Phe	Cys	Ile	Ala	Leu	Gly	Tyr	Thr		
				325					330					335			
aac	agc	tgc	ctc	aac	cca	gtc	ctt	tat	gca	ttt	ctg	gat	gaa	aac	ttc	1056	
Asn	Ser	Cys	Leu	Asn	Pro	Val	Leu	Tyr	Ala	Phe	Leu	Asp	Glu	Asn	Phe		
			340					345					350				

aaa cga tgc ttc aga gag ttc tgt atc cca acc tct tcc aac att gag	1104
Lys Arg Cys Phe Arg Glu Phe Cys Ile Pro Thr Ser Ser Asn Ile Glu	
355 360 365	
caa caa aac tcc act cga att cgt cag aac act aga gac cac ccc tcc	1152
Gln Gln Asn Ser Thr Arg Ile Arg Gln Asn Thr Arg Asp His Pro Ser	
370 375 380	
acg gcc aat aca gtg gat aga act aat cat cag gta cgc agt ctc	1197
Thr Ala Asn Thr Val Asp Arg Thr Asn His Gln Val Arg Ser Leu	
385 390 395	

<210> 16
 <211> 399
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ' Opioid receptor with TEV site in 3rd
 intracellular loop

<400> 16

Met	Asp	Ser	Ser	Ala	Ala	Pro	Thr	Asn	Ala	Ser	Asn	Cys	Thr	Asp	Ala
1				5					10					15	
Leu	Ala	Tyr	Ser	Ser	Cys	Ser	Pro	Ala	Pro	Ser	Pro	Gly	Ser	Trp	Val
			20					25					30		
Asn	Leu	Ser	His	Leu	Asp	Gly	Asp	Leu	Ser	Asp	Pro	Cys	Gly	Pro	Asn
			35				40					45			
Arg	Thr	Asp	Leu	Gly	Gly	Arg	Asp	Ser	Leu	Cys	Pro	Pro	Thr	Gly	Ser
	50					55					60				
Pro	Ser	Met	Ile	Thr	Ala	Ile	Thr	Ile	Met	Ala	Leu	Tyr	Ser	Ile	Val
	65				70				75					80	
Cys	Val	Val	Gly	Leu	Phe	Gly	Asn	Phe	Leu	Val	Met	Tyr	Val	Ile	Val
			85					90					95		
Arg	Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	Asn	Ile	Tyr	Ile	Phe	Asn	Leu
			100					105					110		
Ala	Leu	Ala	Asp	Ala	Leu	Ala	Thr	Ser	Thr	Leu	Pro	Phe	Gln	Ser	Val
		115					120					125			
Asn	Tyr	Leu	Met	Gly	Thr	Trp	Pro	Phe	Gly	Thr	Ile	Leu	Cys	Lys	Ile
	130					135					140				
Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	Phe	Thr	Ser	Ile	Phe	Thr	Leu
	145				150				155					160	
Cys	Thr	Met	Ser	Val	Asp	Arg	Tyr	Ile	Ala	Val	Cys	His	Pro	Val	Lys
			165					170					175		
Ala	Leu	Asp	Phe	Arg	Thr	Pro	Arg	Asn	Ala	Lys	Ile	Ile	Asn	Val	Cys
			180					185					190		
Asn	Trp	Ile	Leu	Ser	Ser	Ala	Ile	Gly	Leu	Pro	Val	Met	Phe	Ile	Ala
	195						200					205			
Thr	Thr	Lys	Tyr	Arg	Gln	Gly	Ser	Ile	Asp	Cys	Thr	Leu	Thr	Phe	Ser
	210					215					220				
His	Pro	Thr	Trp	Tyr	Trp	Glu	Asn	Leu	Leu	Lys	Ile	Cys	Val	Phe	Ile
	225				230					235				240	
Phe	Ala	Phe	Ile	Met	Pro	Val	Leu	Ile	Ile	Thr	Val	Cys	Tyr	Gly	Leu
			245						250					255	
Met	Ile	Leu	Arg	Leu	Lys	Ser	Val	Arg	Met	Leu	Ser	Gly	Ser	Lys	Glu
		260						265					270		
Lys	Asp	Glu	Asn	Leu	Tyr	Phe	Gln	Gly	Arg	Asn	Leu	Arg	Arg	Ile	Thr
		275					280					285			

Arg Met Val Leu Val Val Val Ala Val Phe Ile Val Cys Trp Thr Pro
 290 295 300
 Ile His Ile Tyr Val Ile Ile Lys Ala Leu Val Thr Ile Pro Glu Thr
 305 310 315 320
 Thr Phe Gln Thr Val Ser Trp His Phe Cys Ile Ala Leu Gly Tyr Thr
 325 330 335
 Asn Ser Cys Leu Asn Pro Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe
 340 345 350
 Lys Arg Cys Phe Arg Glu Phe Cys Ile Pro Thr Ser Ser Asn Ile Glu
 355 360 365
 Gln Gln Asn Ser Thr Arg Ile Arg Gln Asn Thr Arg Asp His Pro Ser
 370 375 380
 Thr Ala Asn Thr Val Asp Arg Thr Asn His Gln Val Arg Ser Leu
 385 390 395

<210> 17
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Hemagglutinin tag

<400> 17
 Cys Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 1 5 10

<210> 18
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> c-myc tag

<400> 18
 Cys Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
 1 5 10

<210> 19
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> enterokinase cleavage site

<400> 19
 Asp Asp Asp Asp Lys
 1 5

<210> 20
 <211> 4
 <212> PRT

<213> Artificial Sequence

<220>

<223> factor Xa cleavage site

<400> 20

Ile Glu Gly Arg

1

<210> 21

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> thrombin cleavage site

<400> 21

Leu Val Pro Ala Gly Ser

1

5

<210> 22

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> renin cleavage site

<400> 22

His Pro Phe His Leu Val Ile His

1

5